

Ecological multilayer networks in the microbial world

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Before the seminar we will gather outside of George Evens Family Auditorium. Drinks and snacks will be provided. You are encouraged to bring your own coffee cups. Please join us at 11:45.

Microbial ecology has seen a surge in the use of network theory in the past decade. However, the analysis of multiple dimensions such as variation in space or interconnected networks has been limited. In this talk I will demonstrate how the use of multilayer networks can generate new hypotheses regarding the processes underlying community assembly, considering that structure is a signature for eco-evolutionary processes. In the first example we use sequences-similarity networks to identify potential pathways of gene transmission across interconnected rumen plasmidomes. In the second, we analyze a metacommunity of the rumen microbiome to disentangle the potential role of local (within-community) vs global processes in determining microbe co-occurrence. These two very different examples jointly provide complementary angles for the untapped potential of the application of multilayer networks in microbial ecology.

